

IN THE SPECIFICATION:

Please amend the paragraph beginning on page 29 at line 19 as follows:

Dehalococcoides Ethenogenes Target-specific Primers

Forward Primer DHE 385: (SEQ ID NO:17)

Reverse Primer DHE 807(806): (SEQ ID NO:18)

Detection Probe (Biotin labeled) dD-B DHE 555 B2:

5'BGGCTTAACCGGGACGTGTCATTCAATACBdA 3' (SEQ ID NO:53)

Please amend the paragraph beginning on page 20, line 1 as follows:

(GenBank No. AF004928)[SEQ ID NO:7] was aligned using MEGALIGN (DNASTar, Madison, WI) or Pileup (Genetics Computer Group, Madison, WI) with 16S rRNA sequences from 100 organisms that represent most major domains, families and genera in the major kingdoms of Bacteria and Archaea. The conserved, variable, and highly variable regions could be delineated by boxing off the consensus sequences. Primer candidate sequences were manually picked from the variable and highly variable regions and then their uniqueness was determined by determining their potential as probes to a ribosomal sequence database sequences using the "on-line" Probe Match Program from the Ribosomal Database Project II (<http://www.cme.msu.edu/RDP/html/index.html>) RDPII, Michigan State University, East Lansing, MI). This analysis returned an overview of the matches between a probe and its potential target sequence, as a listing and as a phylogenetic overview. The program results showed the sequences that match the query sequence (if there are such sequences) and also showed sequences that had mismatches, deletions and insertions, citing the number and positions of the aberrations.

Please amend the paragraph beginning on page 6, line 22 as follows:

The term "signature sequence" or "signature sequence region" or "signature groups" will refer to those short sequences in the 16S gene or rRNA molecule which are unique to a certain group or groups of organisms. These sequences can be used to define domains, group, subdivisions genera or species of an organism.

Please amend the paragraph beginning on page 6, beginning at line 2 as follows:

The term "DHE-195" or "DHE (cornell)" will refer to the strains of *Dehalococcoides ethenogenes* isolated and characterized by Maymó-Gatell et al. (*Science*, 176:1568 (1997)).

Please amend the paragraph beginning on page 11, beginning at line 28 as follows:

Although a region similar to that defined by SEQ ID NO:8 is found in the literature sequence, there are significant variations at positions, E184, E190, E197, E200, E207, E216, and E221 as shown below.

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E184	E190	E198 7	E201 0	E208 7	E217 6	E222 1	
TGTGRTGGG	TCY	GACATAW	GTY	GGTTCA	YTAA	AGCCGYAAGGYGC	TTG (SEQ ID NO:8)

With in the context the present invention Applicants have discovered that within the signature region defined by SEQ ID NO:8 above, the R at position E184 may be A/G, the Y at position E190 may be C/T, the W at position ~~E198~~E197 may be A/T, and the Y's at position ~~E201~~E200, ~~E208~~E207, ~~E217~~E216, and ~~E222~~E221 may be T/C.

Please amend the paragraph beginning on page 12, beginning at line 12 as follows:

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Likewise, if the entire 16S rDNA profile is examined, it is seen that there are significant single base differences throughout the entire profile (Figures 1 and 2). These differences are illustrated in tabular form in Table 2. Accordingly a 16S rDNA profile sequence, having the following bases substitutions taken independently or together will be diagnostic for dechlorinating bacteria: E107=G, base E184=G, base E190=C, E ~~198~~197=T, ~~E201~~E200= T, ~~E208~~E207=C, ~~E217~~E216=T, ~~E222~~E221=C, E264=C, E267=C, E291=T, E333= C, E420=C, E444=T, E631=A, E829=A, E933=T, E934=T, E980=C, E1003=T, E1012=T, E1020=G, E1039=A, E1040=C, E1087=T, E1114=C, E1284=T, E1364=T and E1427=A

Please amend Table 2 beginning on page 26 as follows:

TABLE 2

E. coli	DHE No.	DHE-195	Sig. Grp	DHE-PI	DHE-stf	DHE DII	DHE Pin
28	1	1		1	1	1	1
107	66	A 66	6A	A 66	A 66	A 66	G 66
184	144	A 144	2A	A 144	G 144	G 144	G 144
190	150	T 150	2B	T 150	C 150	C 150	C 150
1978	157	A 157	6B	A 157	A 157	A 157	T 157
200+	160	C 160	2C	C 160	T 160	T 160	T 160
2078	167	T 167	2D	T 167	C 167	C 167	C 167
2167	176	C 176	2E	C 176	T 176	T 176	T 176
2212	181	T 181	6C	T 181	T 181	T 181	C 181
264	226	T 226	3A	T 226	C 226	C 226	T 226
267	*229	T 229	1A	C 229	C 229	C 229	C 229
291+	254	d 253+	5A	d 253+	T 254	d 253+	d 253+
333	*296	G 295	1B	C 295	C 296	C 295	C 295
420	383	T 382	3B	T 382	C 383	C 382	T 382
444	407	C 406	6D	C 406	C 407	C 406	T 406
542	*481	G 480	1C	d 479+	d 480+	d 479+	d 479+
631	571	T 570	6E	T 569	T 570	T 569	A 569
829	769	G 768	5B	G 767	A 768	G 767	G 767
933	874	G 873	4A	T 872	G 873	G 872	G 872
934	875	C 874	4B	T 873	C 874	C 873	C 873
980	*921	d 919+	1D	C 919	C 920	C 919	C 919
1003	944	A 942	6F	A 942	A 943	A 942	T 942
1012	955	C 953	6G	C 953	C 954	C 953	T 953
1020	963	A 961	6H	A 961	A 962	A 961	G 961
1039	984	G 982	6I	G 982	G 983	G 982	A 982
1040	985	T 983	6J	T 983	T 984	T 983	C 983
1087	*1033	G 1031	1E	T 1031	T 1032	T 1031	T 1031
1114	*1060	d 1057+	1F	C 1058	C 1059	C 1058	C 1058
1144-56	*1088-96	1086-94	1G	d 1085+	d 1086+	d 1085+	d 1085+
		ACTAGCG AG					
1284	1225	C 1220	3C	C 1213	T 1214	T 1213	C 1213
1364	1304	A 1300	6K	A 1292	A 1293	A 1292	T 1292
1427	1357	N 1353	1H	A 1345	A 1346	A 1346	A 1346

FA